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<110> Daniel Cohen
Ilya Chumakov

<120> Treatment of CNS Disorders Using D-Amino Acid Oxidase and D-Aspartate Oxidase Antagonists

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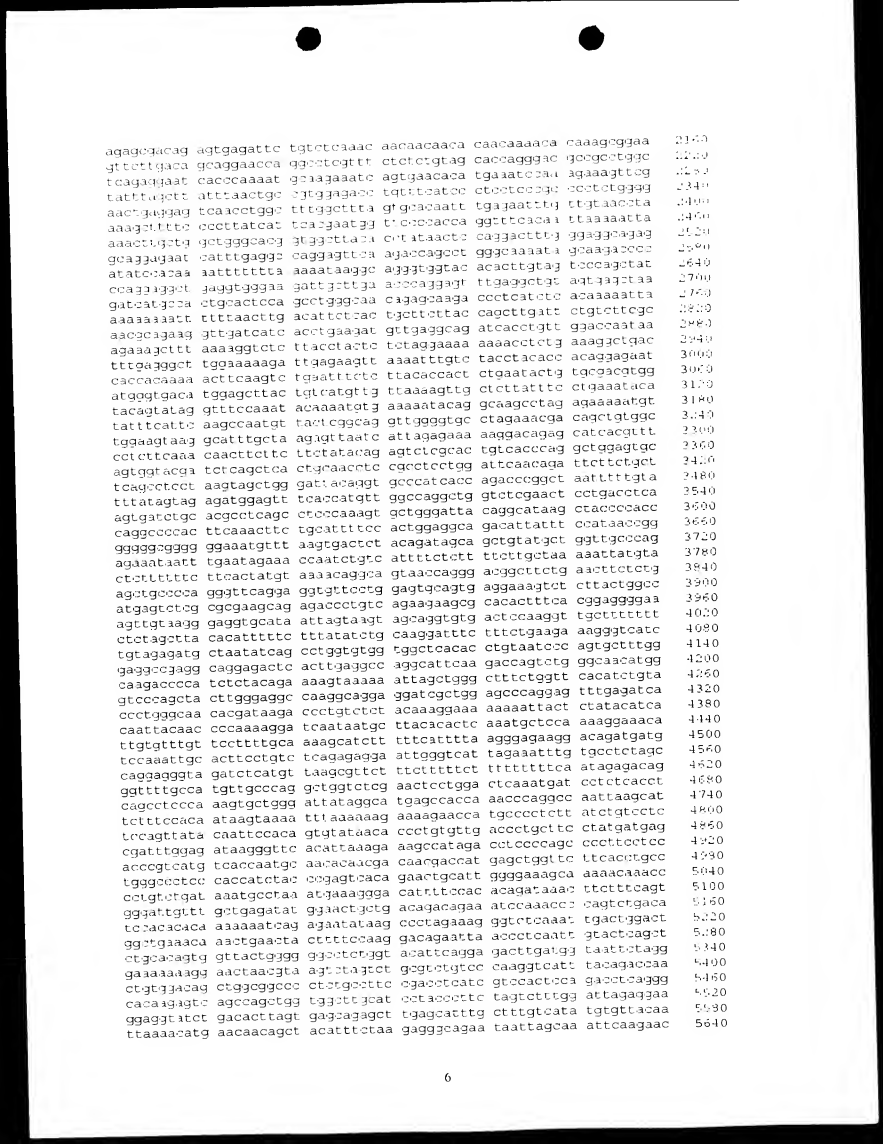

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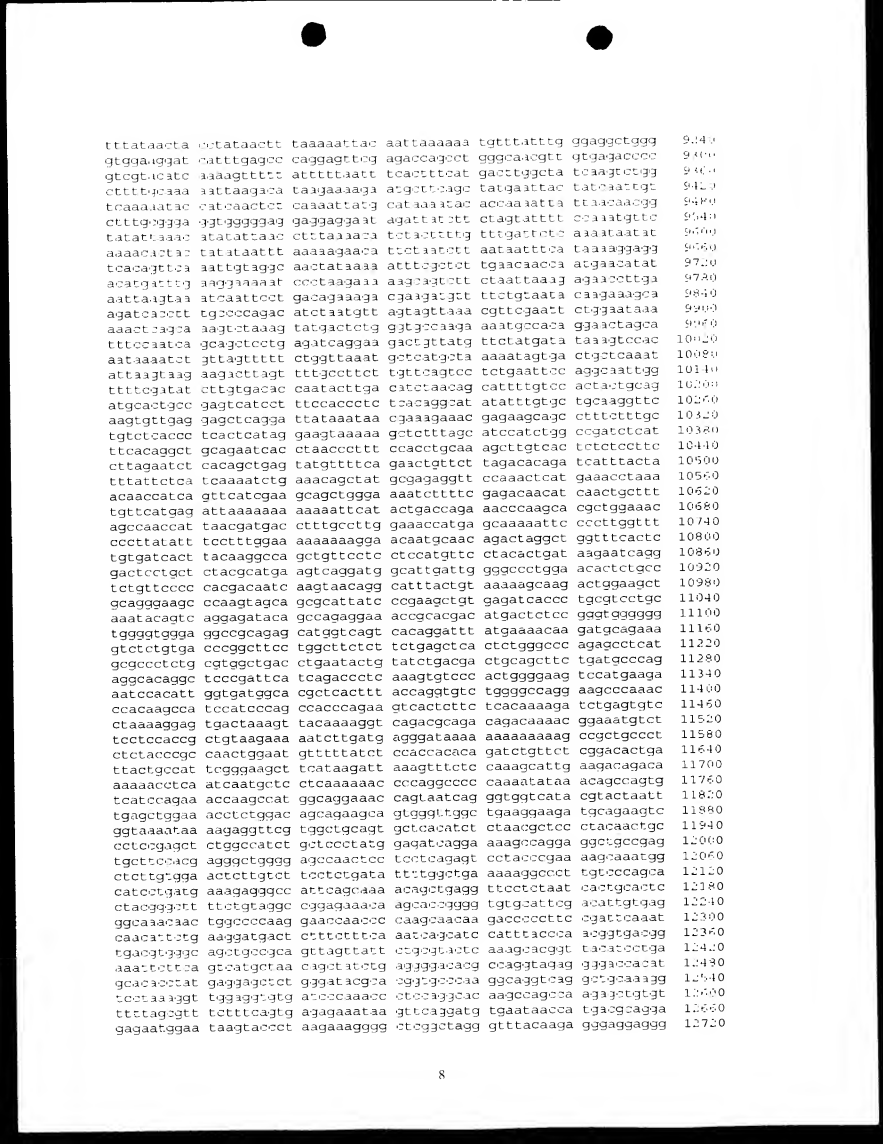

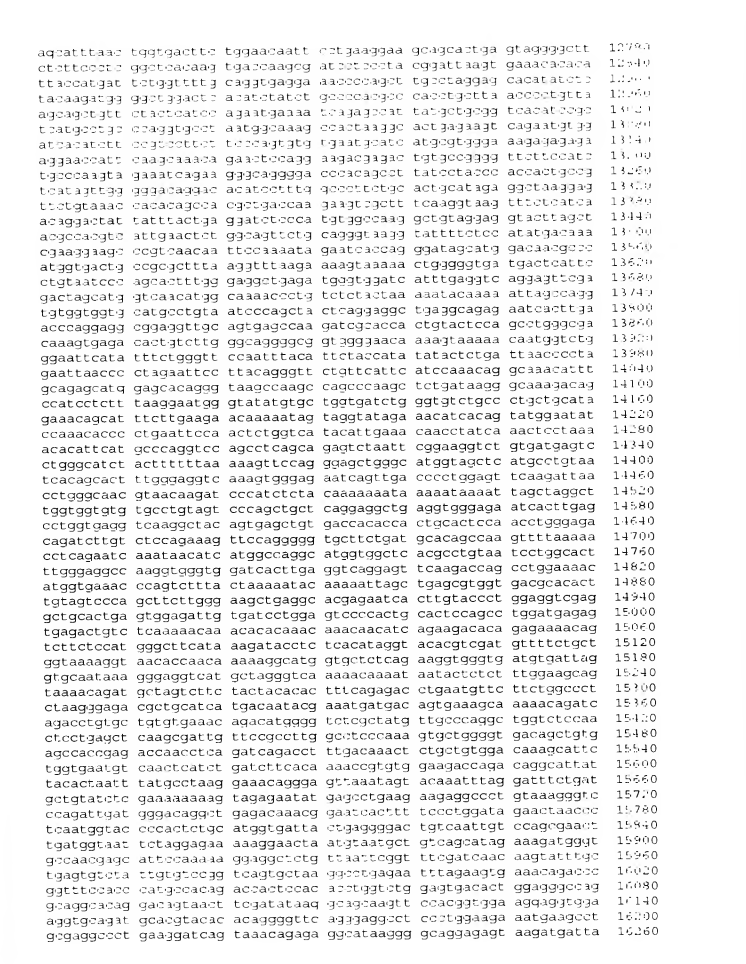

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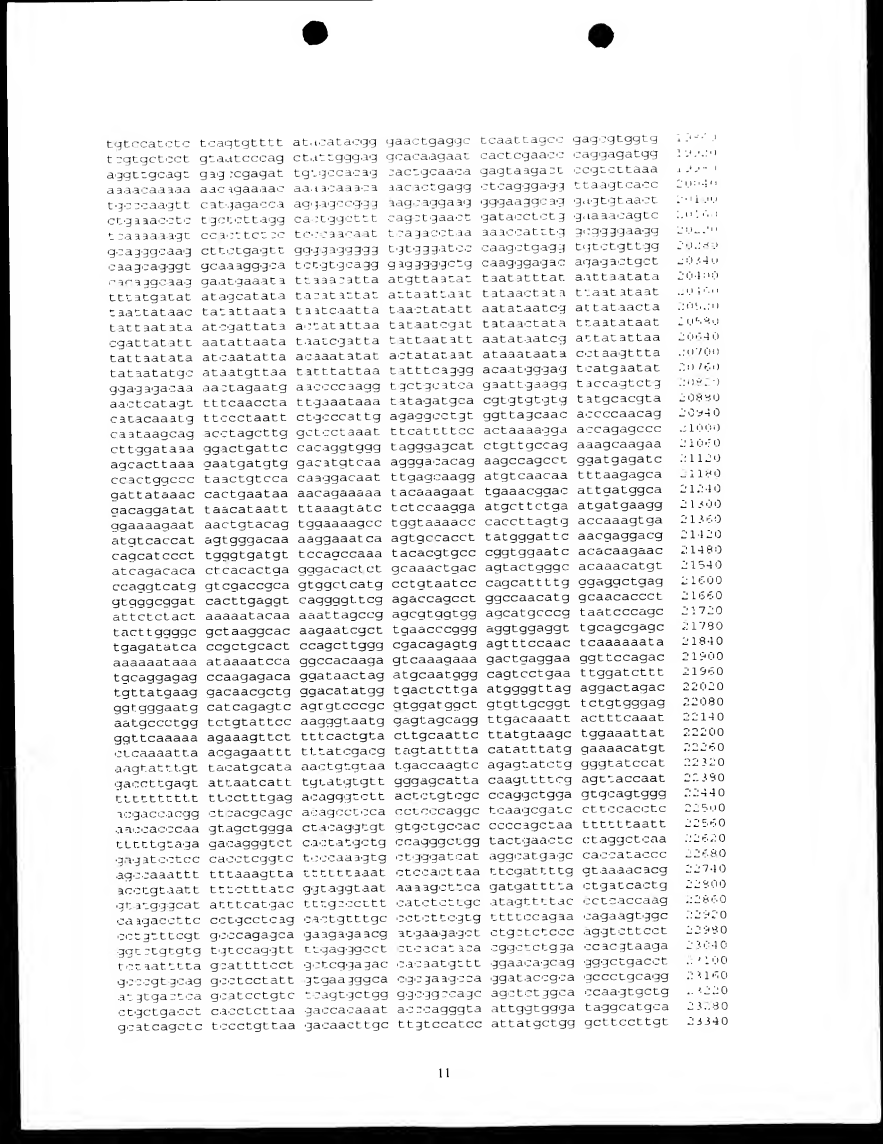

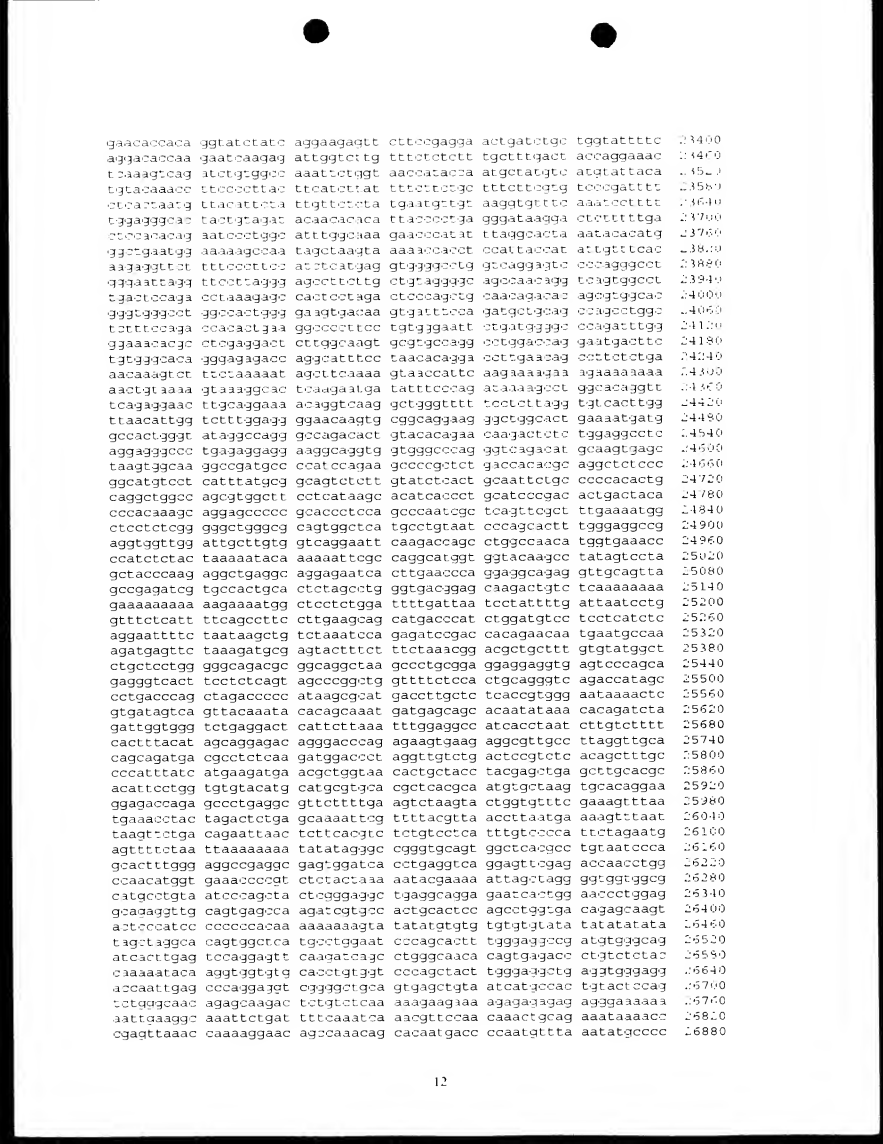

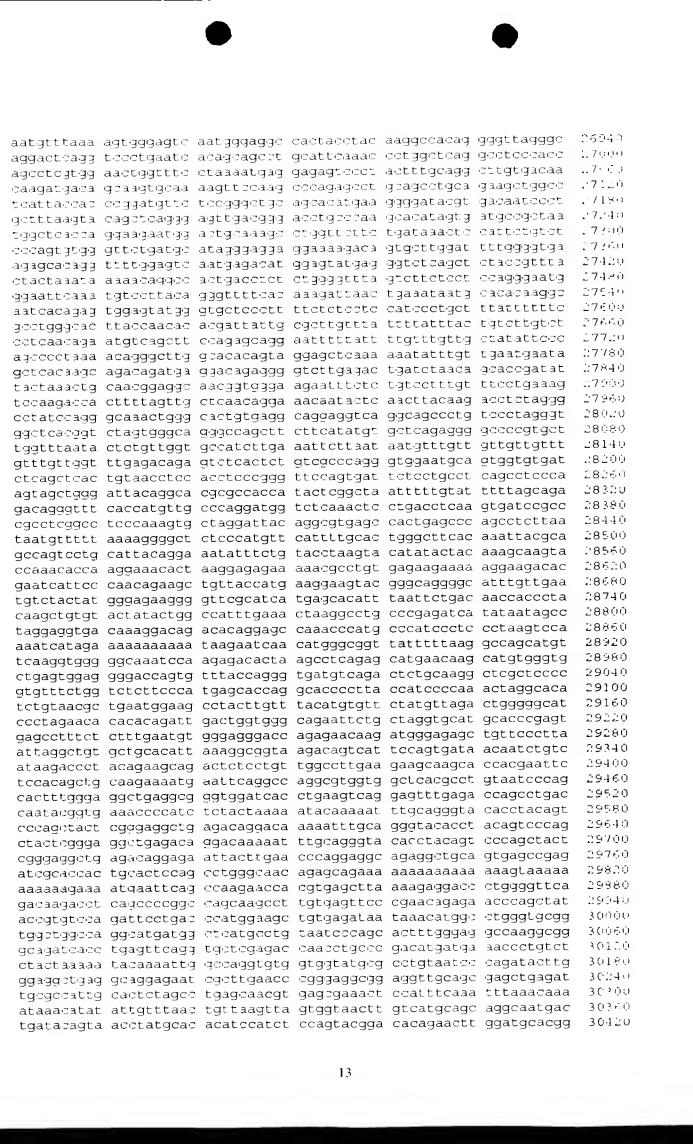
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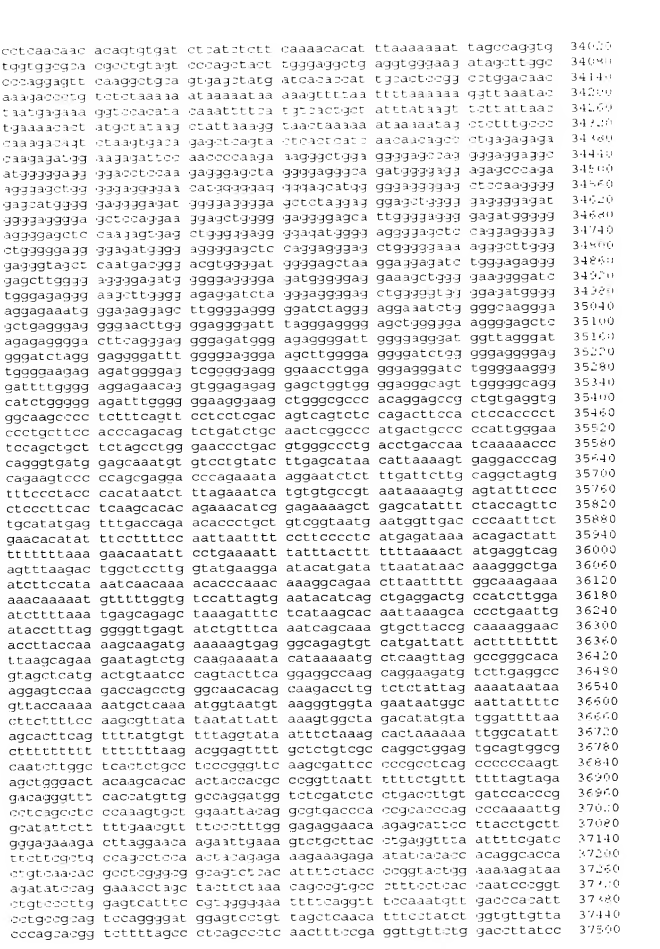

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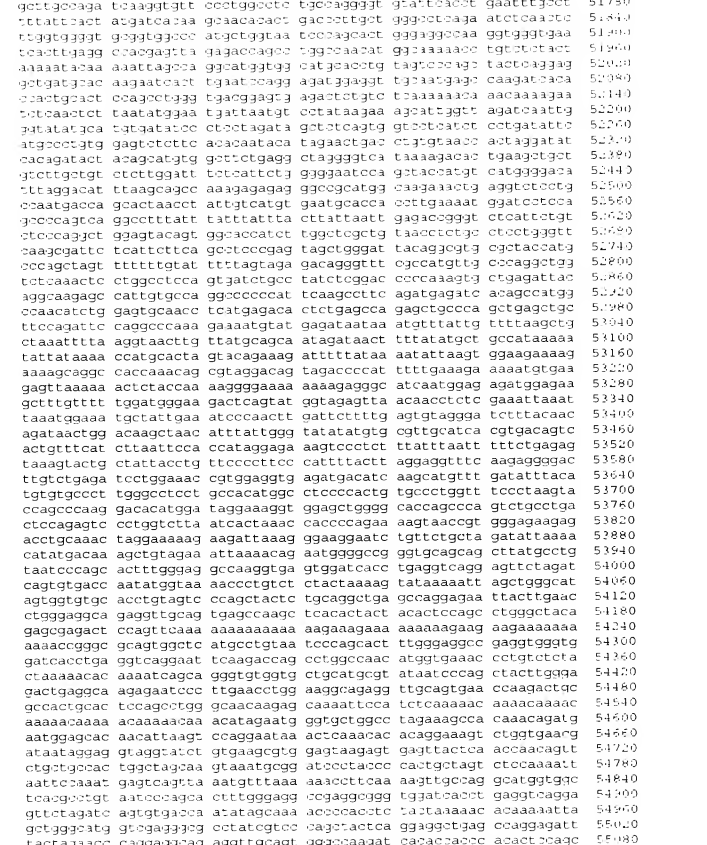

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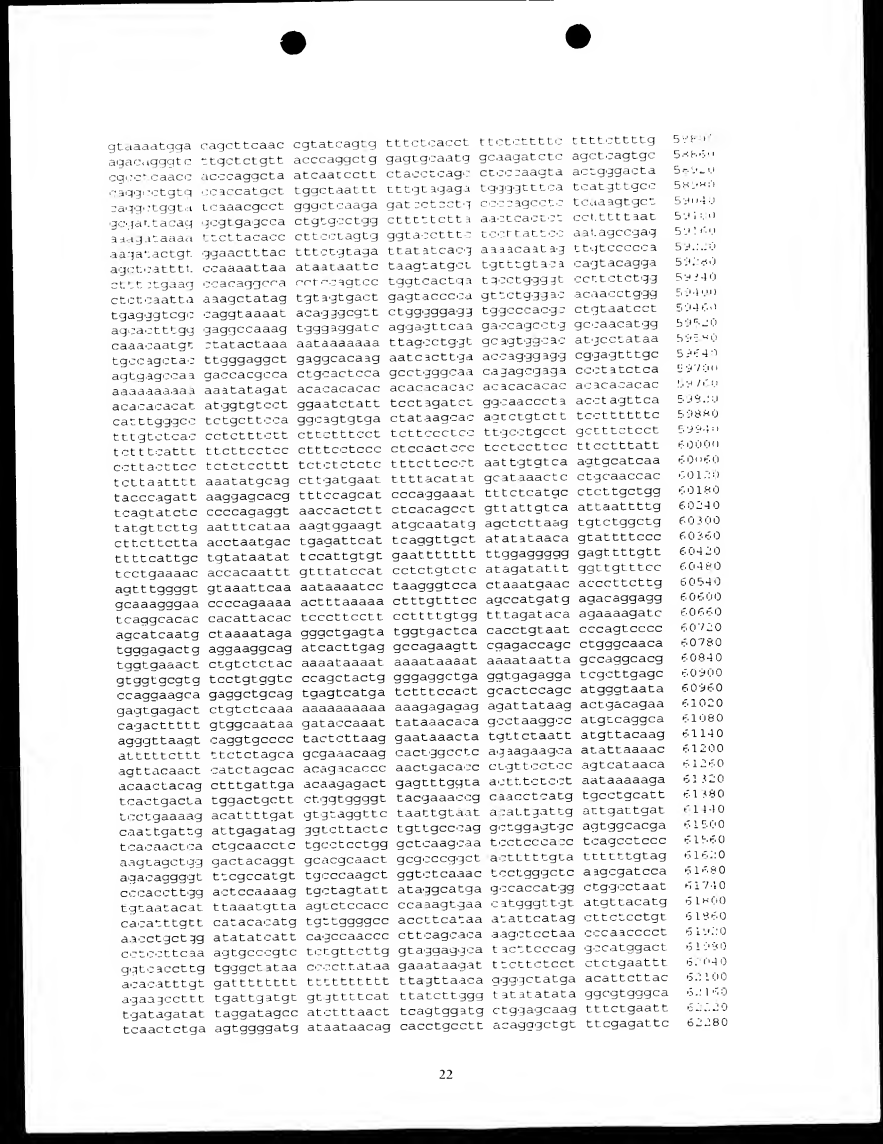

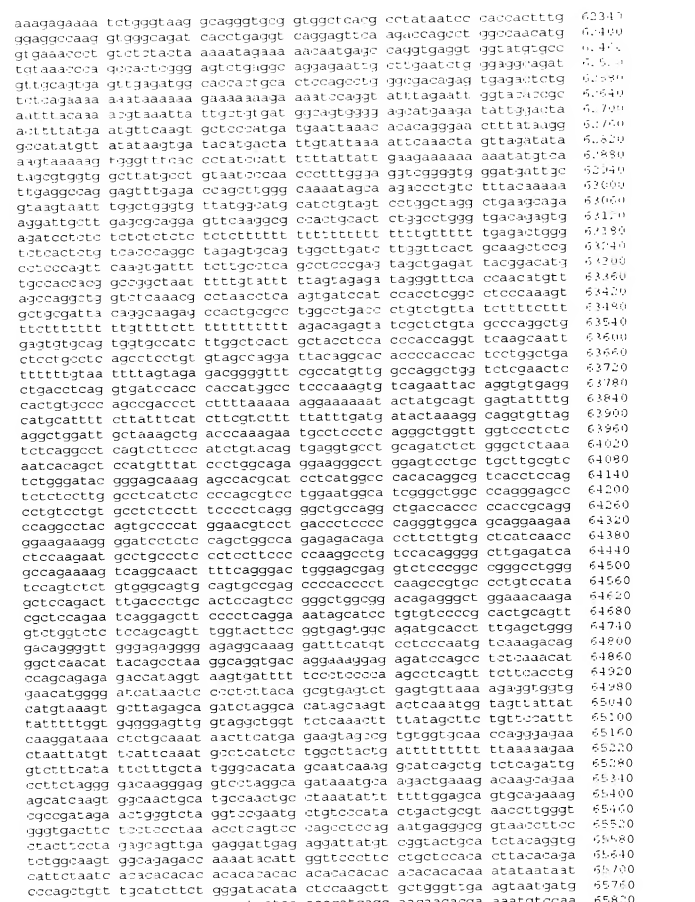

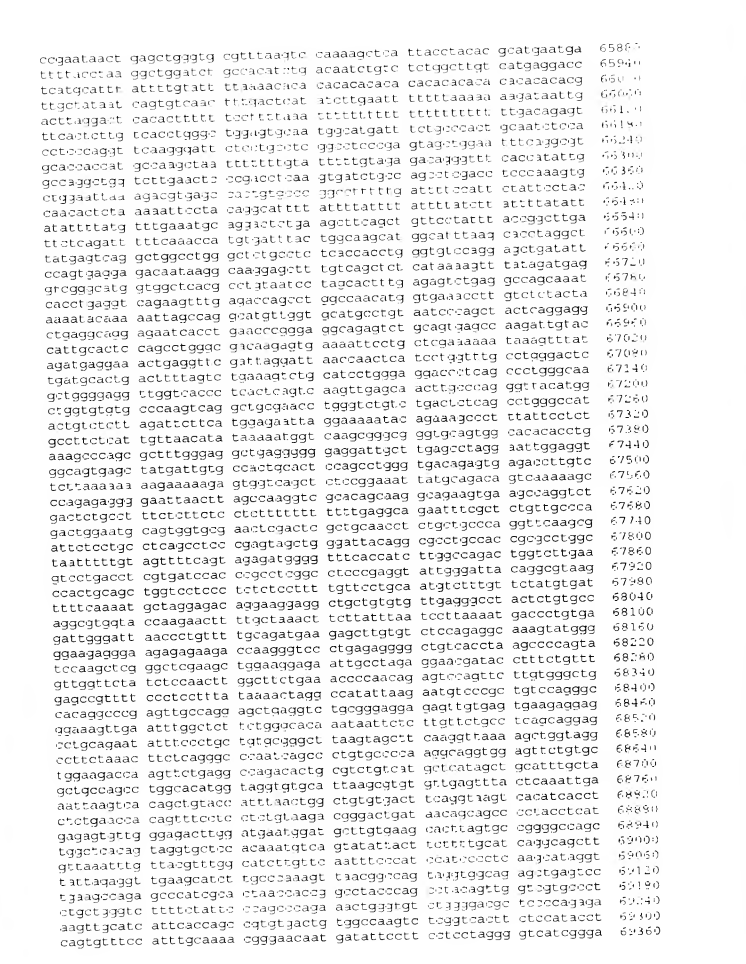

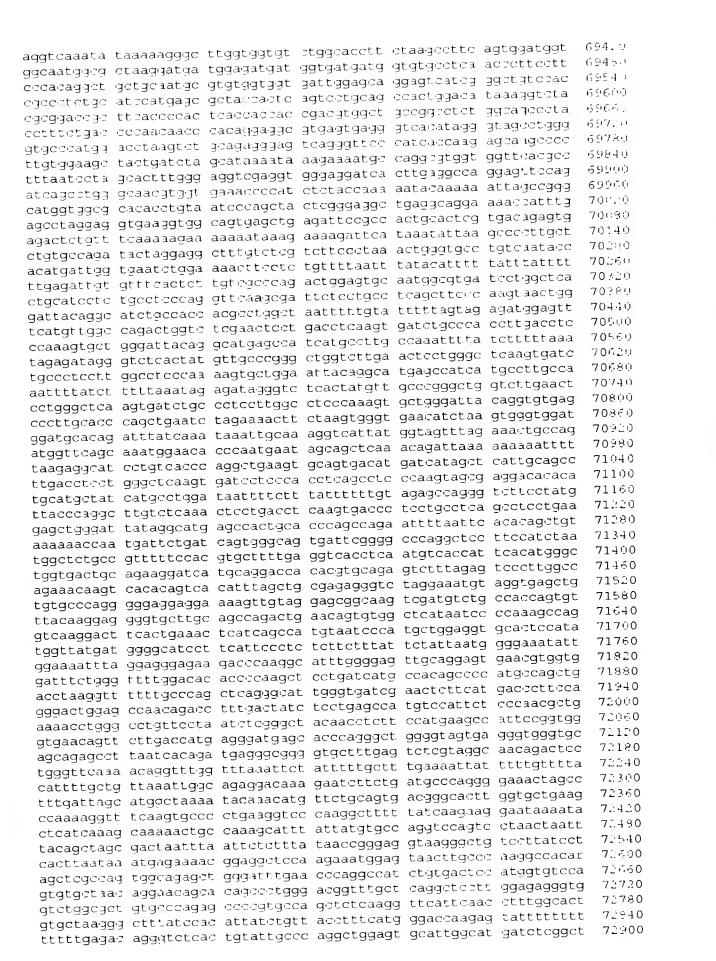

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gtttggtact tccggctgct gca atg cgt gtg gtg gtg att gga gca gga gtc      173
                         Met Arg Val Val Val Ile Gly Ala Gly Val
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Ile Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val
                15                  20                  25
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Leu Gln Pro Leu Asp Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu
            30                  35                  40
acc acc acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac      317
Thr Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp
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ctc ctg agc cat gtc cat tct ccc aac gct gaa aac ctg ggc ctg ttc      413
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75                  80                  85                  90
cta atc tcg ggc tac aac ctc ttc cat gaa gcc att ccg gac cct tcc      461
Leu Ile Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser
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tgg aag gac aca gtt ctg gga ttt cgg aag ctg acc ccc aga gag ctg      509
Trp Lys Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu
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gat atg ttc cca gat tac ggc tat ggc tgg ttc cac aca agc cta att      557
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Leu Glu Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu
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gca aga gaa ggc gca gac gtg att gtc aac tgc act ggg gta tgg gct      701
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Thr Val Thr Leu Gly Gly Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu
295                 300                 305                 310
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Glu Pro Thr Leu Lys Asn Ala Arg Ile Ile Gly Glu Arg Thr Gly Phe
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Arg Pro Val Arg Pro Gln Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr
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375                 380                 385                 390
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Gly Arg Ile Leu Glu Glu Lys Lys Leu Ser Arg Met Pro Pro Ser His
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aaagaagcat gaggtgagag aaagccacaa agtcagtgcc tggagaaggg ttcagcccaa   1354
catggggccc ctctcatcac tgaaatccct ctaccttctc tgggtctggc attataaaga   1414
acagctgagg ctgtcatttc atgagtcttc agaagaaagg acagctcaga aaatcaaaga   1474
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gtttggtact tccggctgct gca atg cgt gtg gtg gtg att gga gca gga gtc     173
                        Met Arg Val Val Val Ile Gly Ala Gly Val
                        1               5                  10
atc ggg ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc      221
Ile Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val
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            30                  35                  40
acc acc acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac      317
Thr Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp
        45                  50                  55
ccc aac aac cca cag gag gcg gac tgg agc caa cag acc ttt gac tat      365
Pro Asn Asn Pro Gln Glu Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr
    60                  65                  70
ctc ctg agc cat gtc cat tct ccc aac gct gaa aac ctg ggc ctg ttc      413
Leu Leu Ser His Val His Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe
75                  80                  85                  90
cta atc tcg ggc tac aac ctc ttc cat gaa gcc att ccg gac cct tcc      461
Leu Ile Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser
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tgg aag gac aca gtt ctg gga ttt cgg aag ctg acc ccc aga gag ctg      509
Trp Lys Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu
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gat atg ttc cca gat tac ggc tat ggc tgg ttc cac aca agc cta att      557
Asp Met Phe Pro Asp Tyr Gly Tyr Gly Trp Phe His Thr Ser Leu Ile
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ctg gag gga aag aac tat cta cag tgg ctg act gaa agg tta act gag      605
Leu Glu Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu
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Arg Gly Val Lys Phe Phe Gln Arg Lys Val Glu Ser Phe Glu Glu Val
155                 160                 165                 170
gca aga gaa ggc gca gac gtg att gtc aac tgc act ggg cta tgg gct      701
Ala Arg Glu Gly Ala Asp Val Ile Val Asn Cys Thr Gly Val Trp Ala
                175                 180                 185
ggg gcg cta caa cga gac ccc ctg ctg cag cca ggc cgg ggg cag atc      749
Gly Ala Leu Gln Arg Asp Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile
            190                 195                 200
atg aag gtg gac gcc cct tgg atg aag cac ttc att ctc acc cat gac      797
Met Lys Val Asp Ala Pro Trp Met Lys His Phe Ile Leu Thr His Asp
        205                 210                 215
cca gag aga ggc atc tac aat tcc ccg tac atc atc cca ggg acc cag      845
Pro Glu Arg Gly Ile Tyr Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln
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Thr Val Thr Leu Gly Gly Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu
235                 240                 245                 250
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Asn Asn Ile Gln Asp His Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu
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gag ccc aca ctg aag aat gca aga att att ggt gaa cga act ggc ttc      989
Glu Pro Thr Leu Lys Asn Ala Arg Ile Ile Gly Glu Arg Thr Gly Phe
            270                 275                 280
cgg cca gta cgc ccc cag att cgg cta gaa aga gaa cag ctt cgc act     1037
Arg Pro Val Arg Pro Gln Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr
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gga cct tca aac aca gag gtc atc cac aac tat ggc cat gga ggc tac     1085
Gly Pro Ser Asn Thr Glu Val Ile His Asn Tyr Gly His Gly Gly Tyr
    300                 305                 310
ggg ctc acc atc cac tgg gga tgt gcc ctg gag gca gcc aag ctc ttt     1133
Gly Leu Thr Ile His Trp Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe
315                 320                 325                 330
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Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln
        15                  20                  25
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Pro Leu Asp Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr
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Asn Pro Gln Glu Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu
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Ser His Val His Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile
            80                  85                  90
tcg ggc tac aac ctc ttc cat gaa gcc att cag gac cct tcc tgg aag      1479
Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys
        95                  100                 105
gac aca gtt ctg gga ttt cgg aag ctg acc tcc aga gag ctg gat atg      1527
Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met
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Phe Pro Asp Tyr Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu
125                 130                 135                 140
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Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly
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        175                 180                 185
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205                 210                 215                 220
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Ile Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val
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acagaaaatg gaggataatt gaggctaagt aacctgatta caagttgtac taacatatta 1437
aaggttctga aaagtcctgc agcaaagaca actatctgat gttgtttaac ccagtgcttg 1497
ctaaacctat ctggctatgg aactcttttg cccagagcac ccatgaatgc catgacacaa 1557
atgctgagaa atgctggaa 1576

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<2222> 114..959

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<222> 1301..1326

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tcctccatgt tattcacagg gtctcagcac gattcatctc aaaggctgct gca atg 116
Met
1
cgt gtg gtg gtg att gga gca gga gtc atc ggg ctg tcc acc gcc ctc 164
Arg Val Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala Leu
5 10 15
tgc atc cat gag cgc tac cac tca gtc ctg cag cca ctg gac ata aag 212
Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile Lys
20 25 30
gtc tac gcg gac cgc ttc acc cca ctc acc acc acc gac gtg gct gcc 260
Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala Ala
35 40 45
ggc ctc tgg cag ccc tac ctt tct gac ccc aac aac cca cag gag gcg 308
Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu Ala
50 55 60 65
gac tgg agc caa cag acc ttt gac tat ctc ctg agc cat gtc cat tct 356
Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His Ser
70 75 80
ccc aac gct gaa aac ctg ggc ctg ttc cta atc tcg ggc tac aac ctc 404
Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn Leu
85 90 95
ttc cat gaa gcc att ccg gtg gca aga gaa ggc gca gac gtg att gtc 452
Phe His Glu Ala Ile Pro Val Ala Arg Glu Gly Ala Asp Val Ile Val
100 105 110
aac tgc act ggg gta tgg gct ggg gcg cta caa cga gac ccc ctg ctg 500
Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp Pro Leu Leu
115 120 125
cag cca ggc cgg ggg cag atc atg aag gtg gac gcc cct tgg atg aag 548
Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro Trp Met Lys
130 135 140 145
cac ttc att ctc acc cat gac cca gag aga ggc atc tac aat tcc cgg 596
His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr Asn Ser Pro
150 155 160
tac atc atc cca ggg acc cag aca gtt act ctt gga ggc atc ttc cag 644
Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly Ile Phe Gln
165 170 175
ttg gga aac tgg agt gaa cta aac aat atc cag gac cac aac acc att 692
Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His Asn Thr Ile
180 185 190
tgg gaa ggc tgc tgc aga ctg gag ccc aca ctg aag aat gca aga att 740
Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn Ala Arg Ile
195 200 205
att ggt gaa cga act ggc ttc cgg cca gta cgc ccc cag att cgg cta 788
Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln Ile Arg Leu
210 215 220 225
gaa aga gaa cag ctt cgc act gga cct tca aac aca gag gtc atc cac 836
Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu Val Ile His

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                230                 235                 240
aac tat ggc cat gga ggc tac ggg ctc acc atc cac tgg gga tgt gcc      884
Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp Gly Cys Ala
            245                 250                 255
ctg gag gca gcc aag ctc trt ggg aga atc ctg gaa gaa aag aaa ttg      932
Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu Lys Lys Leu
        260                 265                 270
tcc aga atg cca cca tcc cac ctc tgaagactcc agtgactgct gcctcccccc      986
Ser Arg Met Pro Pro Ser His Leu
    275                 280
acaagaactc cctctcccc tcagccaatg aatcaatgtg ctcctcata agccattgct     1046
tctcccttac ttctttcctc aaagaagcat gaggtgagag aaagccacaa agtcagtgcc     1106
tggagaaggg ttcagcccaa catgggggcc ctctcatcac tgaaatcccc ctacctttct     1166
tgggtctggc attataaaga acagctgagg ctgtcattcc atgagtcttc agtagaaagg     1226
acagctcaga aaatcaaaga ggccaactgc ccagagccac agaaaatgga ggataattga     1286
ggctaagtaa cctgattaca agttgtacta acatattaaa ggttctgaaa agtcctgca      1345

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<212> PRT
<213> Homo sapiens

<400> 7
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Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
            20                  25                  30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
        35                  40                  45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
    50                  55                  60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65                  70                  75                  80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
                85                  90                  95
Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys Asp Thr Val Leu
            100                 105                 110
Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met Phe Pro Asp Tyr
        115                 120                 125
Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu Gly Lys Asn Tyr
    130                 135                 140
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe
145                 150                 155                 160
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp
                165                 170                 175
Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp
            180                 185                 190
Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro
        195                 200                 205
Trp Met Lys His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr
    210                 215                 220
Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly
225                 230                 235                 240
Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His
                245                 250                 255
Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn
            260                 265                 270
Ala Arg Ile Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln
        275                 280                 285
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Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu
290 295 300
Val Ile His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp
305 310 315 320
Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu
325 330 335
Lys Lys Leu Ser Arg Met Pro Pro Ser His Leu
340 345

<210> 8
<211> 220
<212> PRT
<213> Homo sapiens

<400> 8
Met Arg Val Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala
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Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
20 25 30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
35 40 45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
50 55 60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65 70 75 80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
85 90 95
Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys Asp Thr Val Leu
100 105 110
Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met Phe Pro Asp Tyr
115 120 125
Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu Gly Lys Asn Tyr
130 135 140
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe
145 150 155 160
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp
165 170 175
Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp
180 185 190
Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Asp Pro Asp Ser
195 200 205
Tyr Ser Trp Arg His Leu Pro Val Gly Lys Leu Glu
210 215 220

<210> 9
<211> 78
<212> PRT
<213> Homo sapiens

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Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
20 25 30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
35 40 45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
50 55 60
Ala Thr Leu Pro Gly Arg Thr Gln Phe Trp Asp Phe Gly Ser

65 70 75

<210> 10
<211> 281
<212> PRT
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20 25 30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
35 40 45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
50 55 60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65 70 75 80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
85 90 95
Leu Phe His Glu Ala Ile Pro Val Ala Arg Glu Gly Ala Asp Val Ile
100 105 110
Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp Pro Leu
115 120 125
Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro Trp Met
130 135 140
Lys His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr Asn Ser
145 150 155 160
Pro Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly Ile Phe
165 170 175
Gln Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His Asn Thr
180 185 190
Ile Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn Ala Arg
195 200 205
Ile Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln Ile Arg
210 215 220
Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu Val Ile
225 230 235 240
His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp Gly Cys
245 250 255
Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu Lys Lys
260 265 270
Leu Ser Arg Met Pro Pro Ser His Leu
275 280

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<211> 456
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<223> 99-16105-152 : polymorphic base A or G

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<223> 99-16105-152.probe

<220>
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<222> 133..151
<223> 99-16105-152.mis

<220>
<221> primer_bind
<222> 153..171
<223> 99-16105-152.mis complement

<220>
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<222> 1..19
<223> 99-16105.pu

<220>
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<222> 437..456
<223> 99-16105.rp complement

<400> 11
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cgaaataaga agctctttag caatttactt tggatattgg ttttcttttg aaggacagtt 120
attaaaatag cttgtaggat tactcatttt crttttttctt ctttttaaat ataaagcaat 180
gtcatcactt ttttccctgt attatatttc tcctcaataa ttgatatgct acattaaagg 240
aacacaaaat ggtcttaatt atgcaataat gatcaaggca aagagtgttt cctgggaact 300
aatggttgcc tgagaggagg tgatggcttg aggtccagct ggttattaag ccgcaggaaa 360
tgctgcaggc caagatttgt attatttctc tgagatgaaa atgaacccaa aaaaaggcaa 420
aatgggtttt tctccactaa tgggtaaaat gaactc 456

<210> 12
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 215
<223> 99-5919-215 : polymorphic base A or G

<220>
<221> misc_binding
<222> 203..227
<223> 99-5919-215.probe

<220>
<221> primer_bind
<222> 196..214
<223> 99-5919-215.mis

<220>
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<222> 216..234
<223> 99-5919-215.mis complement

<220>
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<222> 11..29

<223> 99-5919.pu

<220>
<221> primer_bind
<222> 445..465
<223> 99-5919.rp complement

<400> 13
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agtccacaaa atcacctttt cctgtataca ttttaggat gtcagacttt attctaatga 180
ttttcccttag ttgcccccca aaattgtatt ctacrgtgtg attttaaagc tgaattttca 240
aaatgatatt tcatatctat attttcacaa gcttttcttc tatgaatgtt attgtcagct 300
gtcaagggtgt gagatggtac ttgatactac attctttcca agctgttgcc tgaatcggtt 360
taaaacaaag tcattactag gctgtaaact gttgctctgc aaaattgagc agcacgtatt 420
taaccactca tacttcttag ctctccaaca ctttgagtcr ata 463

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<212> DNA
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<222> 1..46

<220>
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<222> 47..508

<220>
<221> 3'UTR
<222> 509..742

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<222> 718..723

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<222> 21
<223> 8-135 112 : polymorphic base C or T

<220>
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<222> 75
<223> 8-135-166 : polymorphic base A or C

<220>
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<222> 135
<223> 99-16038-118 : polymorphic base A or G

<220>
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<222> 194
<223> 8-137-152 : polymorphic base G or T

<220>

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<222> 224
<223> 8-137-182 : polymorphic base A or G

<220>
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<222> 390
<223> 8-130-220 : polymorphic base A or C

<220>
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<222> 406
<223> 8-130-236 : polymorphic base A or G

<220>
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<223> 8-131-199 : polymorphic base A or C

<220>
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<222> 641
<223> 8-132-97 : polymorphic base C or T

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<222> 708
<223> 8-132-164 : polymorphic base C or T

<220>
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<222> 723
<223> 8-132-179 : polymorphic base A or T

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<220>
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<222> 135
<223> Xaa=Lys or Arg

<220>
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<222> 194
<223> Xaa=Glu or Stop

<220>
<221> VARIANT
<222> 224
<223> Xaa=Gly or Arg

<220>
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<223> Xaa=Ala or Asp

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Lys Leu Met Gly Ala Asp Xaa Leu Gln Leu Phe Arg Ser Arg Tyr Thr
5 10 15
ttg ggt aaa atc tac ttc ata ggt ttt caa arg agc att ctt ctg agc 151
Leu Gly Lys Ile Tyr Phe Ile Gly Phe Gln Xaa Ser Ile Leu Leu Ser
20 25 30 35
aaa tct gaa aac tct cta aac tct att gca aag gag aca gaa kaa gga 199
Lys Ser Glu Asn Ser Leu Asn Ser Ile Ala Lys Glu Thr Glu Xaa Gly
40 45 50
aga gag acg gta aca agg aaa gaa rga tgg aag aga agg cat gag gac 247
Arg Glu Thr Val Thr Arg Lys Glu Xaa Trp Lys Arg Arg His Glu Asp
55 60 65
ggc tat ttg gaa atg gca cag agg cat tta cag aga tca tta tgt cct 295
Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser Leu Cys Pro
70 75 80
tgg gtc tct tac ctt cct cag ccc tat gca gag ctt gaa gaa gta agc 343
Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu Glu Val Ser
85 90 95
agc cat gtt gga aaa gtc ttc atg gca aga aac tat gag ttc ctt gmc 391
Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu Phe Leu Xaa
100 105 110 115
tat gag gcc tct aar gac cgc agg cag cct cta gaa cga atg tgg acc 439
Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg Met Trp Thr
120 125 130
tgc aac tac aac cag caa aaa gac cag tca tgc aac cac aag gaa ata 487
Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His Lys Glu Ile
135 140 145
act tct acc aaa gct gaa tgagtttgga agcagattct tcccagccaa 535
Thr Ser Thr Lys Ala Glu
150
tccttctgat gacaatgtag tctggccaac atcttcactg gamtctgacg gactctgtgt 595
ctgggaccca gctgataaca cgtggtgatg ggattgtatt tgcaaytctc tggtcagtaa 655
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ttattaawtg tgcttcaagt tttaaca 742

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<211> 153
<212> PRT
<213> Homo sapiens

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<223> Xaa=Ser or Tyr

<220>
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<222> 30
<223> Xaa=Lys or Arg

<220>
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<222> 50
<223> Xaa=Glu or Stop

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<222> 60
<223> Xaa=Gly or Arg

<220>
<221> VARIANT
<222> 115
<223> Xaa=Ala or Asp

<220>
<221> SITE
<222> 63..64
<223> basic protease cleavage site

<220>
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<222> 122..123
<223> basic protease cleavage site

<220>
<221> DISULFID
<222> 132..142

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<222> 65..123

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Arg Tyr Thr Leu Gly Lys Ile Tyr Phe Ile Gly Phe Gln Xaa Ser Ile
20 25 30
Leu Leu Ser Lys Ser Glu Asn Ser Leu Asn Ser Ile Ala Lys Glu Thr
35 40 45
Glu Xaa Gly Arg Glu Thr Val Thr Arg Lys Glu Xaa Trp Lys Arg Arg
50 55 60
His Glu Asp Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser
65 70 75 80
Leu Cys Pro Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu
85 90 95
Gln Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
100 105 110
Phe Leu Xaa Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
115 120 125
Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
130 135 140
Lys Glu Ile Thr Ser Thr Lys Ala Glu
145 150

<210> 15

<211> 476
<212> DNA
<213> Homo sapiens

<400> 15
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His Glu Asp Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser
1 5 10 15
tta tgt cct tgg gtc tct tac ctt cct cag ccc tat gca gag ctt gaa 96
Leu Cys Pro Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu
20 25 30
gaa gta agc agc cat gtt gga aaa gtc ttc atg gca aga aac tat gag 144
Glu Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
35 40 45
ttc ctt gcc tat gag gcc tct aag gac cgc agg cag cct cta gaa cga 192
Phe Leu Ala Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
50 55 60
arg tgg acc tgc aac tac aac cag caa aaa gac cag tca tgc aac cac 240
Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
65 70 75 80
aag gaa ata act tct acc aaa gct gaa tgagtttgga agcagattct 287
Lys Glu Ile Thr Ser Thr Lys Ala Glu
85
tccagccaa tcttctgat gacaatgtag tctggccaac atcttcactg gactctgacg 347
gactctgtgt ctgggaccca gctgataaca cgtggtgatg ggattgtatt tgcaactctc 407
tggtcagtaa gtgataaaat gccatttcta tgcacccacc tggcctgtgt gactgggaga 467
atctctctt 476

<210> 16
<211> 89
<212> PRT
<213> Homo sapiens

<400> 16
His Glu Asp Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser
1 5 10 15
Leu Cys Pro Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu
20 25 30
Glu Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
35 40 45
Phe Leu Ala Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
50 55 60
Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
65 70 75 80
Lys Glu Ile Thr Ser Thr Lys Ala Glu
85

<210> 17
<211> 1533
<212> DNA
<213> Homo sapiens

<400> 17
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tgggtgcacg tggaaggcgg acagagggct ggaaacaaga cgctccagaa tcaggagctt 120
cccctcagga aatagcatcc tgtgtccccg cactgcagtt gtctggtctc tccagcagtt 180
tggtacttcc ggctgctgca atg cgt gtg gtg gtg att gga gca gga gtc atc 233
Met Arg Val Val Val Ile Gly Ala Gly Val Ile
1 5 10

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ggg ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc ctg      281
Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val Leu
            15                  20                  25
cag cca ctg cac ata aag gtc tac gcg gac cgc ttc acc gca ctc acc      329
Gln Pro Leu His Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr
        30                  35                  40
acc acc gac gtg gct gcc gac ctc tgg cag ccc tac ctt tct gac ccc      377
Thr Thr Asp Val Ala Ala Asp Leu Trp Gln Pro Tyr Leu Ser Asp Pro
    45                  50                  55
aac aac cca cag gag gtg gac tgg agc caa cag acc ttt gac tat ctc      425
Asn Asn Pro Gln Glu Val Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu
60                  65                  70                  75
ctg agc cat gtc cat tct ccc aac gct gaa aac ctg ggc ctg ttc cta      473
Leu Ser His Val His Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu
                80                  85                  90
atc tcg ggc tac aac ctc ttc cat gaa gcc att ccg gac cct tcc tgg      521
Ile Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp
            95                  100                 105
aag gac aca gtt ctg gga ttt cgg aag ctg acc ccc aga gag ctg gat      569
Lys Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp
        110                 115                 120
atg ttc cca gat tac ggc tat ggc tgg ttc cac aca agc cta att ctg      617
Met Phe Pro Asp Tyr Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu
    125                 130                 135
gag gga aag aac tat cta cag tgg ctg act gaa agg tta act gag agg      665
Glu Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg
140                 145                 150                 155
gga gtg aag ttc ttc cag cgg aaa gtg gag tct ttt gag gag gtg gca      713
Gly Val Lys Phe Phe Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala
                160                 165                 170
aga gaa ggc gca gac gtg att gtc aac tgc act ggg gta tgg gct ggg      761
Arg Glu Gly Ala Asp Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly
            175                 180                 185
gcg cta caa cga gac ccc ctg ctg cag cca ggc cgg ggg cag atc atg      809
Ala Leu Gln Arg Asp Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met
        190                 195                 200
aag gtg gac gcc cct tgg atg aag cac ttc att ctc acc cat gac cca      857
Lys Val Asp Ala Pro Trp Met Lys His Phe Ile Leu Thr His Asp Pro
    205                 210                 215
gag aga ggc atc tac aat tcc ccg tac atc atc cca ggg acc cag aca      905
Glu Arg Gly Ile Tyr Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln Thr
220                 225                 230                 235
gtt act ctt gga ggc atc ttc cag ttg gga aac tgg agt gaa cta aac      953
Val Thr Leu Gly Gly Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu Asn
                240                 245                 250
aat atc cag gac cac aac acc att tgg gaa ggc tgc tgc aga ctg gag     1001
Asn Ile Gln Asp His Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu Glu
            255                 260                 265
ccc aca ctg aag aat gca aga att att ggt gaa gca act ggc ttc cgg     1049
Pro Thr Leu Lys Asn Ala Arg Ile Ile Gly Glu Ala Thr Gly Phe Arg
        270                 275                 280
cca gta cgc ccc cag att cgg cta gaa aga gaa cag ctt cgc act gga     1097
Pro Val Arg Pro Gln Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr Gly
    285                 290                 295
cct tca aac aca gag gtc atc cac aac tat ggc cat gga ggc tac ggg     1145
Pro Ser Asn Thr Glu Val Ile His Asn Tyr Gly His Gly Gly Tyr Gly
300                 305                 310                 315
ctc acc atc cac tgg gga tgt gcc ctg gag gca gcc aag ctc ttt ggg     1193
Leu Thr Ile His Trp Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe Gly
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                320                 325                 330
aga atc ctg gaa gaa aag aaa ttg tcc aga atg cca cca tcc cac ctc     1241
Arg Ile Leu Glu Glu Lys Lys Leu Ser Arg Met Pro Pro Ser His Leu
            335                 340                 345
tgaagactcc agtgactgct gcctcccccc acaagaactc cctctcccca tcagccaatg   1301
aatcaatgtg ctccttcata agccattgct tctcctcac ttttttcctc aaagaagcat    1361
gaggtgagag aaagccacra agtcagtgcc tggagaaagg ttcagcccaa catggggccc   1421
ctctcatcac tgaaatccct ctacctttcc tgggtctggc attataaaga acagctgagg   1481
gtgtcattcc atgagtcttc agaagaaagg acagctcaga aagtcaaaga ggccaactgc   1541
ccaaagccac aqaaaaatgga qqataattga qqctaagtaa cctgattaca agttgtacta   1601
acatattaaa ggttctgaaa agtcctgcaa aa                                 1633

<210> 18
<211> 347
<212> PRT
<213> Homo sapiens

<400> 18
Met Arg Val Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala
1               5                   10                  15
Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
            20                  25                  30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
        35                  40                  45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
    50                  55                  60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65                  70                  75                  80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
                85                  90                  95
Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys Asp Thr Val Leu
            100                 105                 110
Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met Phe Pro Asp Tyr
        115                 120                 125
Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu Gly Lys Asn Tyr
    130                 135                 140
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe
145                 150                 155                 160
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp
                165                 170                 175
Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp
            180                 185                 190
Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro
        195                 200                 205
Trp Met Lys His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr
    210                 215                 220
Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly
225                 230                 235                 240
Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His
                245                 250                 255
Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn
            260                 265                 270
Ala Arg Ile Ile Gly Glu Ala Thr Gly Phe Arg Pro Val Arg Pro Gln
        275                 280                 285
Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu
    290                 295                 300
Val Ile His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp
305                 310                 315                 320
Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu
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                325                 330                 335
Lys Lys Leu Ser Arg Met Pro Pro Ser His Leu
            340                 345

<210> 19
<211> 1200
<212> DNA
<213> Homo sapiens

<400> 19
atg gac aca gca cgg att gca gtt gtc ggg gca ggt gtg gtg ggg ctc      48
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1               5                   10                  15
tcc acg gct gtg tgc atc tcc aaa ctg gtg ccc cga tgc tcc gtt acc      96
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
            20                  25                  30
atc att tca gac aag ttt act cca gat tcc acc agt gat gtg gca gcc     144
Ile Ile Ser Asp Lys Phe Thr Pro Asp Ser Thr Ser Asp Val Ala Ala
        35                  40                  45
gga atg ctt att cct cac act tat cca gat aca ccc att cac acg cag     192
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
    50                  55                  60
aag cag tgg ttc aga gaa acc ttt aat cac ctc ttt gca att gcc aat     240
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                  70                  75                  80
tct gca gaa gct gga gat gct ggt gtt cat ttg gta tca ggt tgg cag     288
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Trp Gln
                85                  90                  95
ata ttt cag agc act ccg act gaa gaa gtg cca ttc tgg gct gac gtg     336
Ile Phe Gln Ser Thr Pro Thr Glu Glu Val Pro Phe Trp Ala Asp Val
            100                 105                 110
gtt ctg gga ttt cga aag atg act gag gct gag ctg aag gaa ttc ccc     384
Val Leu Gly Phe Arg Lys Met Thr Glu Ala Glu Leu Lys Lys Phe Pro
        115                 120                 125
cag tat gtg ttt ggt cag gct ttt aca acc ctg aaa tgt gaa tgc cct     432
Gln Tyr Val Phe Gly Gln Ala Phe Thr Thr Leu Lys Cys Glu Cys Pro
    130                 135                 140
gcc tac ctc ccg tgg ttg gag aaa agg ata aag gga agt gga ggc tgg     480
Ala Tyr Leu Pro Trp Leu Glu Lys Arg Ile Lys Gly Ser Gly Gly Trp
145                 150                 155                 160
aca ctc act cgg cga ata gaa gac ctg tgg gaa ctt cat ccg tcc ttt     528
Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu Leu His Pro Ser Phe
                165                 170                 175
gac atc gtg gtc aac tgt tca ggc ctt gga agc aga cag ctt gca gga     576
Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser Arg Gln Leu Ala Gly
            180                 185                 190
gac tca aag att ttc cct gta agg ggc caa gtc ctc caa gtt cag gct     624
Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val Leu Gln Val Gln Ala
        195                 200                 205
ccc tgg gtg gag cat ttt atc cga gat ggc agt ggg ctg aca tat att     672
Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser Gly Leu Thr Tyr Ile
    210                 215                 220
tat cct ggt aca tcc cat gta acc cta ggt gga act agg caa aaa ggg     720
Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly Thr Arg Gln Lys Gly
225                 230                 235                 240
gac tgg aat ctg tcc ccg gat gca gaa aat agc aga gag att ctt tcc     768
Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser Arg Glu Ile Leu Ser
                245                 250                 255
cga tgc tgt gct ctg gag ccc tcc ctc caa gga gcc tgc aac atc agg     816
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Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly Ala Cys Asn Ile Arg
            260                 265                 270
gag aag gtg ggc ttg agg ccc tac agg cca ggc gtg cga ctg cag aca      864
Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly Val Arg Leu Gln Thr
        275                 280                 285
gag ctc ttt ggg cga gat gga cag agg ctg cct gta gtc cac cac tat      912
Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro Val Val His His Tyr
    290                 295                 300
ggc cat ggg agt ggg ggc atc tca gtg cac tgg ggc act gct ctg gag      960
Gly His Gly Ser Gly Gly Ile Ser Val His Trp Gly Thr Ala Leu Glu
305                 310                 315                 320
gcc gcc agg ctg gtg agc gag tgt gtc cat gcc ctc agg acc ccc att     1008
Ala Ala Arg Leu Val Ser Glu Cys Val His Ala Leu Arg Thr Pro Ile
                325                 330                 335
ccc aag tca aac ctg tagatgacat aaaatgacag caaagagact gagagactgt     1063
Pro Lys Ser Asn Leu
            340
tgatcaaagc acagaacagg ttcaaataac ttttccactg catgaaagtt taattagaca    1123
tttctttgtt ttcaacatta gaagtggtgt aacatgtaag ctgagcacgg tagcatgcct    1183
atagtcccag ctacttg                                                  1200

<210> 20
<211> 1023
<212> DNA
<213> Homo sapiens

<400> 20
atg gac aca gca cgg att gca gtt gtc ggg gca ggt gtg gtg ggg ctc       48
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1               5                   10                  15
tcc acg gct gtg tgc atc tcc aaa ctg gtg ccc cga tgc tcc gtt acc       96
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
            20                  25                  30
atc att tca gac aag ttt act cca gat acc acc agt gat gtg gca gcc      144
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
        35                  40                  45
gga atg ctt att cct cac act tat cca gat aca ccc att cac acg cag      192
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
    50                  55                  60
aag cag tgg ttc aga gaa acc ttt aat cac ctc ttt gca att gcc aat      240
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                  70                  75                  80
tct gca gaa gct gga gat gct ggt gtt cat ttg gta tca ggg ata aag      288
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Ile Lys
                85                  90                  95
gga agt gga ggc tgg aca ctc act cgg cga ata gaa gac ctg tgg gaa      336
Gly Ser Gly Gly Trp Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu
            100                 105                 110
ctt cat ccg tcc ttt gac atc gtg gtc aac tgt tca ggc ctt gga agc      384
Leu His Pro Ser Phe Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser
        115                 120                 125
aga cag ctt gca gga gac tca aag att ttc cct gta agg ggc caa gtc      432
Arg Gln Leu Ala Gly Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val
    130                 135                 140
ctc caa gtt cag gct ccc tgg gtg gag cat ttt atc cga gat ggc agt      480
Leu Gln Val Gln Ala Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser
145                 150                 155                 160
ggg ctg aca tat att tat cct ggt aca tcc cat gta acc cta ggt gga      528
Gly Leu Thr Tyr Ile Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly
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                    165                 170                 175
act agg caa aaa ggg gac tgg aat ctg tcc ccg gat gca gaa aat agc      576
Thr Arg Gln Lys Gly Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser
            180                 185                 190
aga gag att ctt tct cga tgc tgt gct ctg gag ccc tcc ctc cac gga      624
Arg Glu Ile Leu Ser Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly
        195                 200                 205
gcc tgc aac atc agg gag aag gtg ggc ttg agg ccc tac agg cca ggc      672
Ala Cys Asn Ile Arg Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly
    210                 215                 220
gtg cga ctg cag aca gag ctc ctt gcg cga gat gga cag agg ctg cct      720
Val Arg Leu Gln Thr Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro
225                 230                 235                 240
gta gtc cac cac tat ggc cat ggg agt ggg ggc atc tca gtg cac tgg      768
Val Val His His Tyr Gly His Gly Ser Gly Gly Ile Ser Val His Trp
                245                 250                 255
ggc act gct ctg gag gcc gcc agg ctg gtg agc gag tgt gtc cat gcc      816
Gly Thr Ala Leu Glu Ala Ala Arg Leu Val Ser Glu Cys Val His Ala
            260                 265                 270
ctc agg acc ccc att ccc aag tca aac ctg tagatgacat aaaatgacag       866
Leu Arg Thr Pro Ile Pro Lys Ser Asn Leu
        275                 280
caaagagact gagagactgt tgatcaaagc acagaacagg ttcaaataac ttttcactg    926
catgaaagtt taattagaca tttctttgtt ttcaacatta gaagtggtgt aacatgtaag    986
ctgagcacgg tagcatgcct atagtcccag ctatttg                           1023

<210> 21
<211> 341
<212> PRT
<213> Homo sapiens

<400> 21
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1               5                   10                  15
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
            20                  25                  30
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
        35                  40                  45
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
    50                  55                  60
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                  70                  75                  80
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Trp Gln
                85                  90                  95
Ile Phe Gln Ser Thr Pro Thr Glu Glu Val Pro Phe Trp Ala Asp Val
            100                 105                 110
Val Leu Gly Phe Arg Lys Met Thr Glu Ala Glu Leu Lys Lys Phe Pro
        115                 120                 125
Gln Tyr Val Phe Gly Gln Ala Phe Thr Thr Leu Lys Cys Glu Cys Pro
    130                 135                 140
Ala Tyr Leu Pro Trp Leu Glu Lys Arg Ile Lys Gly Ser Gly Gly Trp
145                 150                 155                 160
Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu Leu His Pro Ser Phe
                165                 170                 175
Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser Arg Gln Leu Ala Gly
            180                 185                 190
Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val Leu Gln Val Gln Ala
        195                 200                 205
Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser Gly Leu Thr Tyr Ile
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    210                 215                 220
Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly Thr Arg Gln Lys Gly
225                 230                 235                 240
Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser Arg Glu Ile Leu Ser
                245                 250                 255
Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly Ala Cys Asn Ile Arg
            260                 265                 270
Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly Val Arg Leu Gln Thr
        275                 280                 285
Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro Val Val His His Tyr
    290                 295                 300
Gly His Gly Ser Gly Gly Ile Ser Val His Trp Gly Thr Ala Leu Glu
305                 310                 315                 320
Ala Ala Arg Leu Val Ser Glu Cys Val His Ala Leu Arg Thr Pro Ile
                325                 330                 335
Pro Lys Ser Asn Leu
            340
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<210> 22
<211> 282
<212> PRT
<213> Homo sapiens

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<400> 22
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1               5                   10                  15
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
            20                  25                  30
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
        35                  40                  45
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
    50                  55                  60
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                  70                  75                  80
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Ile Lys
                85                  90                  95
Gly Ser Gly Gly Trp Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu
            100                 105                 110
Leu His Pro Ser Phe Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser
        115                 120                 125
Arg Gln Leu Ala Gly Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val
    130                 135                 140
Leu Gln Val Gln Ala Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser
145                 150                 155                 160
Gly Leu Thr Tyr Ile Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly
                165                 170                 175
Thr Arg Gln Lys Gly Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser
            180                 185                 190
Arg Glu Ile Leu Ser Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly
        195                 200                 205
Ala Cys Asn Ile Arg Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly
    210                 215                 220
Val Arg Leu Gln Thr Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro
225                 230                 235                 240
Val Val His His Tyr Gly His Gly Ser Gly Gly Ile Ser Val His Trp
                245                 250                 255
Gly Thr Ala Leu Glu Ala Ala Arg Leu Val Ser Glu Cys Val His Ala
            260                 265                 270
Leu Arg Thr Pro Ile Pro Lys Ser Asn Leu
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275 280

<210> 23
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide 24-1443-126

<220>
<221> allele
<222> 24
<223> polymorphic base C or T

<400> 23
taaggcttag taagttggag nacyaggatc agaagacagg tctgcct 47

<210> 24
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide 24-1457-52

<220>
<221> allele
<222> 24
<223> polymorphic base C or A

<400> 24
tctgagatgc ccctgtgtcc tctmagggag tagtggctga gcatttc 47

<210> 25
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide 27-93-181

<220>
<221> allele
<222> 24
<223> polymorphic base C or T

<400> 25
ccccagcctctg ccactggcga rctytgtggc cttgggcaag ttactcc 47

<210> 26
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide 24-1461-256

<220>

<221> allele
<222> 24
<223> polymorphic base A or G

<400> 26
gatggctctg gcattttcag ggarcagtca tgtctgatct caagttc 47
1